

Figure S1: Phylogenetic trees of partial (762 nucleotides from the 3' end) RdRp sequences of all norovirus P-groups with GIV (red font) and GVI (blue font) strains cluster together and therefore are not divided into distinct GIV and GIV P-types. The phylogenetic analysis was carried out using maximum likelihood (ML) with PhyML. GI and GII P-group sequences are collapsed for clarity.

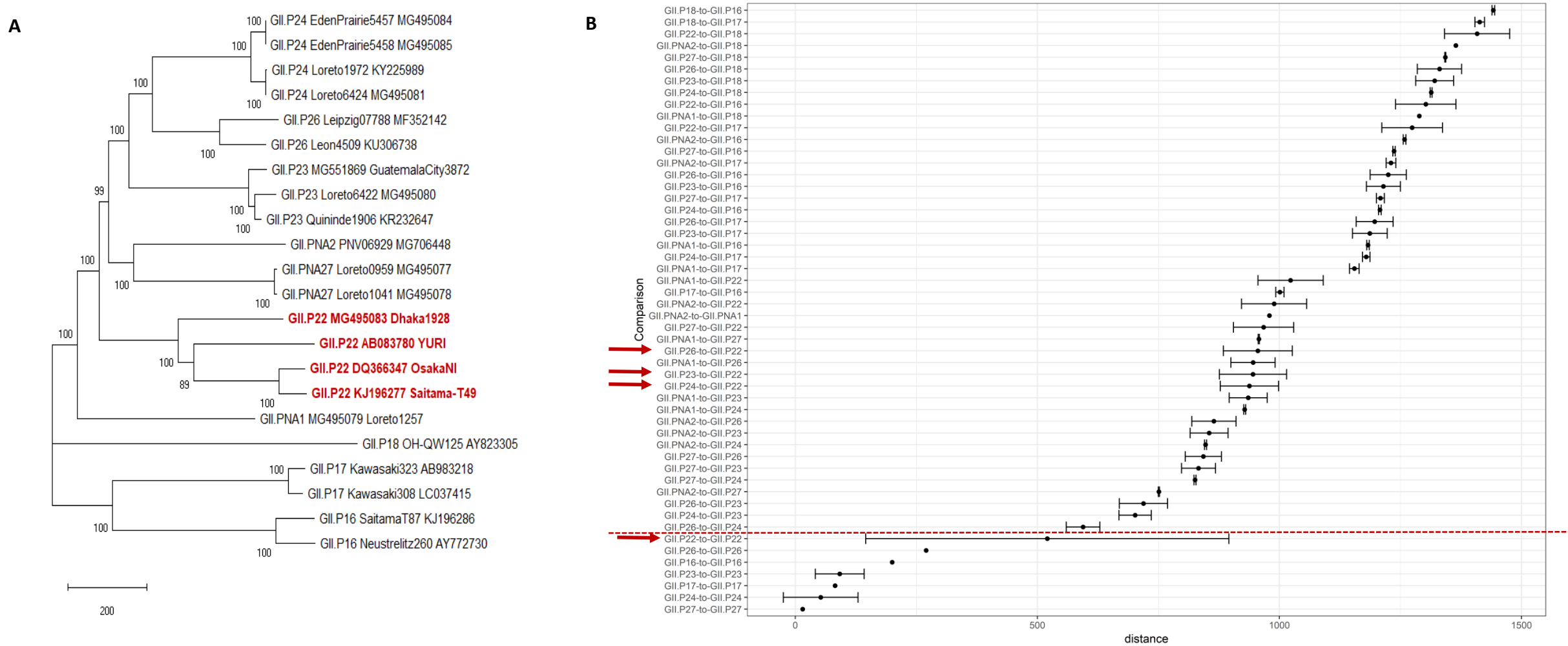


Figure S2: A) Phylogenetic tree of complete ORF1 nucleotide sequences of GII.P22 viruses (highlighted in red) with its phylogenetically closest P-types. The phylogenetic analysis was carried out using maximum likelihood (ML) with PhyML. B) Patristic and P-distance comparison of GII.P16, GII.P17, GII.P18, GII.P22, GII.P23, GII.P24, GII.P25, GII.P26, GII.P27, GII.PNA1 and GII.PNA2 P-types. The error bars represent ± 2 SDs for each P-type comparison. The red arrows indicate the overlap of $2 \times \text{SD}$ error bars for distances of viruses within GII.P22 cluster and between GII.P22 and GII.P23, GII.P22 and GII.P24 and GII.P22 and GII.P26 clusters. Below the dotted line within P-type distances are indicated and above the dotted line distances between P-types are indicated.

$2 \times \text{SD}$ criterion: Phylogenetic distances of sequences within a P-type should not overlap with distances of sequences between different P-types.

Note: To satisfy $2 \times \text{SD}$ criteria, GII.P22 strains were divided into GII.P22, GII.P40 and GII.PNA5 P-types.

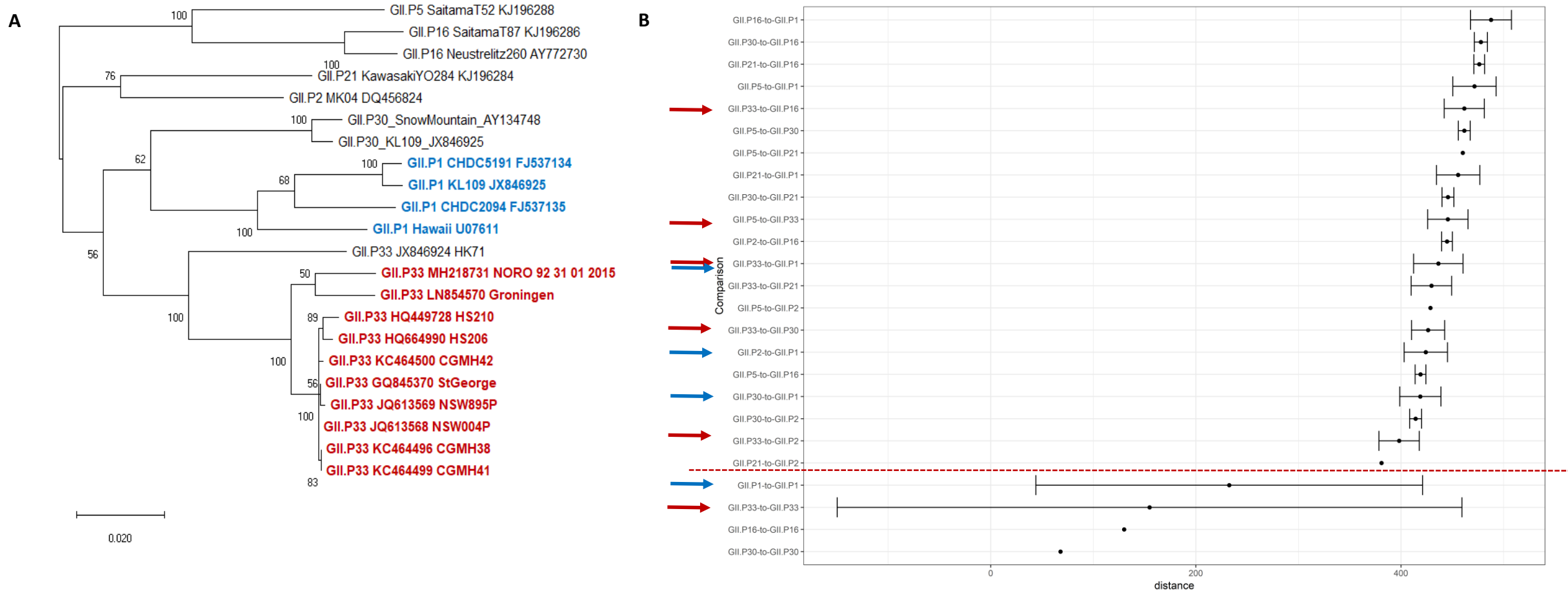


Figure S3: A) Phylogenetic tree of complete ORF1 nucleotide sequences GII.P1 (highlighted in blue) and GII.P33 (previously GII.Pg) strains (highlighted in red) with phylogenetically closer P-types GII.P5, GII.P16, GII.P21, GII.P2 and GII.P30 (previously GII.Pc). The phylogenetic analysis was carried using maximum likelihood (ML) with PhyML. B) Patristic and P-distance comparison of GII.P1 and GII.P33 strains. The error bars represent ± 2 SDs for each P-type comparison. The blue arrows indicate the overlap of $2 \times \text{SD}$ error bars for distances of viruses within GII.P1 cluster and between GII.P1 and GII.P2, GII.P1 and GII.P30 and GII.P1 and GII.P33 cluster. The red arrows indicate the overlap of $2 \times \text{SD}$ error bars for distances of viruses within GII.P33 cluster and between GII.P33 and GII.P1, GII.P33 and GII.P2, GII.P33 and GII.P5, GII.P33 and GII.P16 and GII.P33 and GII.P30 clusters. Below the dotted line within P-type distances are indicated and above the dotted line distances between P-types are indicated.

$2 \times \text{SD}$ criterion: Phylogenetic distances of sequences within a P-type should not overlap with distances between different P-types.

Note: To satisfy $2 \times \text{SD}$ criteria, GII.P1 strains were divided into GII.P1, GII.P39 and GII.PNA3 and GII.33 strains were divided into GII.P33 and GII.P41 P-types.

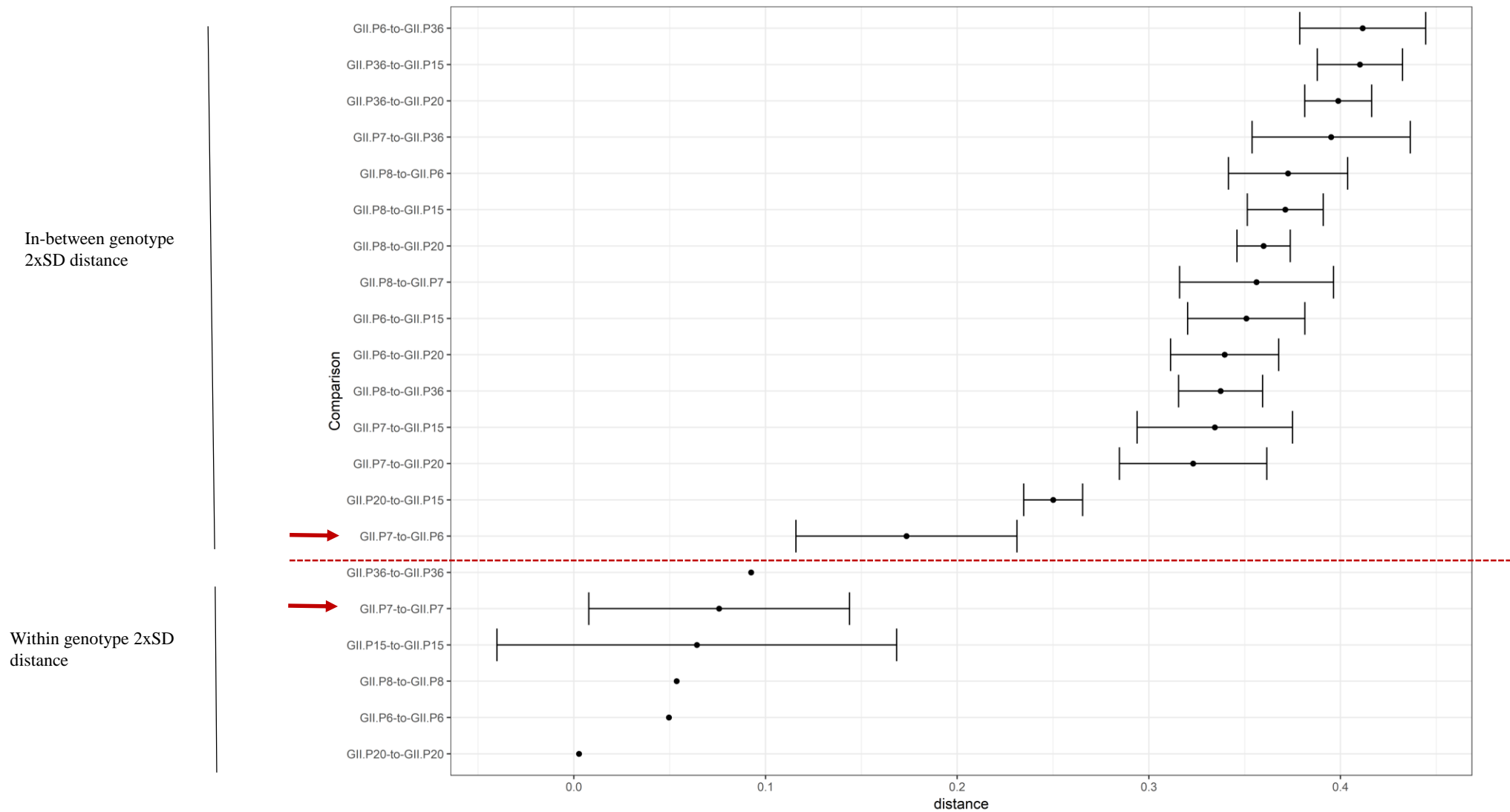


Figure S4: Patristic and P-distance comparison of GII.P6 and GII.P7 strains with phylogenetically closer P-types GII.P8, GII.P15, GII.P20 and GII.36 (previously GII.Pk). The error bars represent ± 2 SDs for each P-type comparison. The red arrows indicate the overlap of 2xSD error bars representing distance within GII.P7 cluster and between GII.P7 and GII.P6 clusters. Below the dotted line within P-type distances are indicated and above the dotted line distances between P-types are indicated.

2xSD criteria: Phylogenetic distances of sequences within a P-type should not overlap with distances of sequences between different P-types.

Note: Although GII.P6 and GII.P7 clusters did not meet 2xSD criteria for classification, we decided not to merge them in a single P-type to avoid confusion with the published literature.

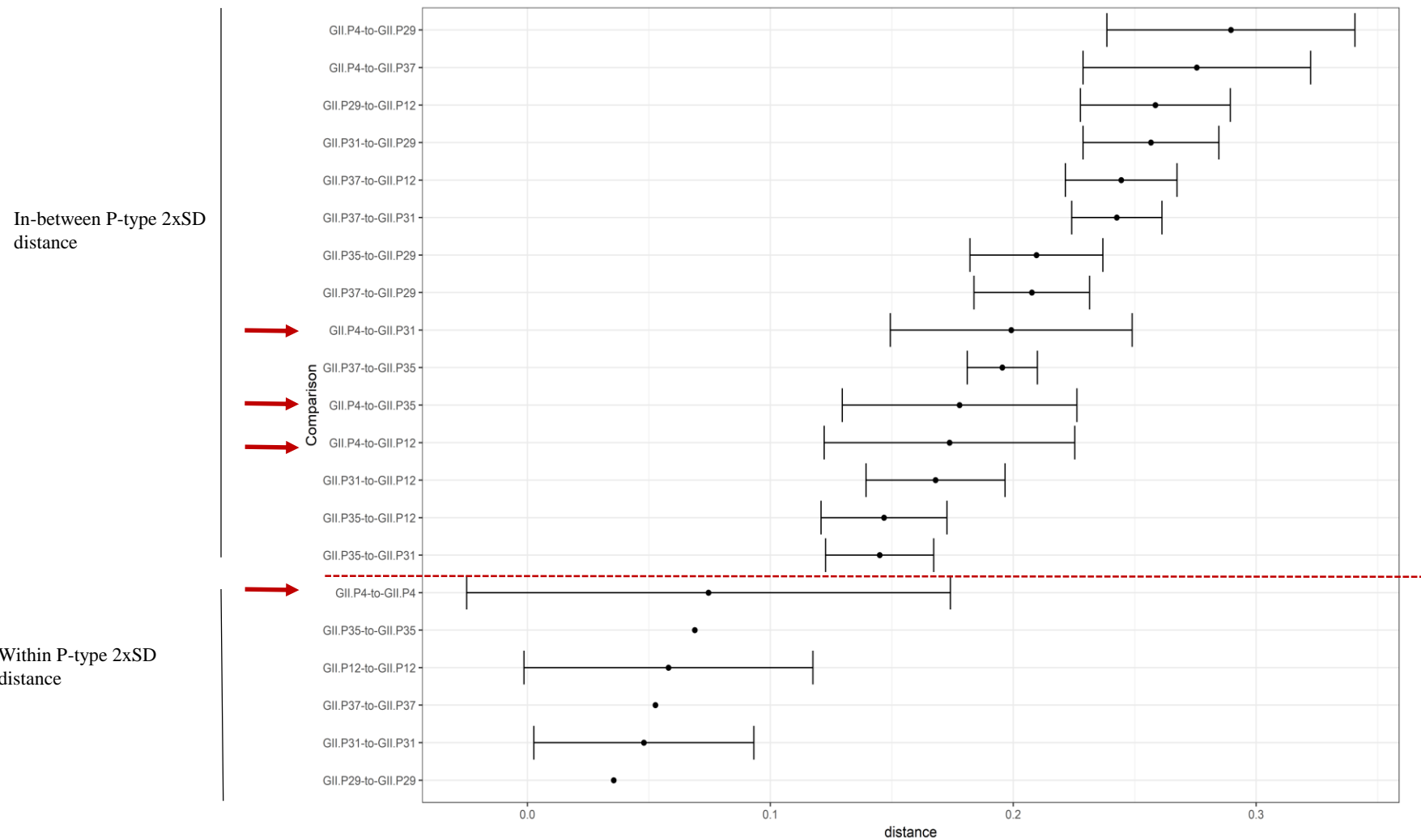


Figure S5: Patristic and P-distance comparison of GII.P4 strains with phylogenetically closest P-types GII.P12, GII.P31 (previously GII.Pe), GII.P35 (previously GII.Pj), GII.P37 (previously GII.Pm), and GII.P29 (previously GII.Pa). The error bars represent ± 2 SDs for each P-type comparison. The red arrows indicate the overlap of 2xSD error bars representing distance within GII.P4 cluster and between GII.P4 and GII.P12, GII.P4 and GII.P31 and GII.P4 and GII.P35 clusters. Below the dotted line within P-type distances are indicated and above the dotted line distances between P-types are indicated.

2xSD criteria: Phylogenetic distances of sequences within a P-type should not overlap with distances between different P-types.

Note: Although GII.P4 strains did not satisfy 2xSD criteria for classification, due to their epidemiologic importance and historic relevance (e.g., GII.P31, previously GII.Pe), we decided not to assign new or merge existing P-types.